

From: Gibbs, Terra  
Sent: Friday, September 13, 2002 1:40 PM  
To: STIC-Biotech/ChemLib  
Subject: SEQ Search

Could you please search SEQ ID NO: 3 of serial number 10/008789

Please do a length limited search of 50 nucleotides or less. Also no EST's.

Terra Gibbs #79523  
AU 1635  
Mailbox 11E12  
306-3221

THANK YOU!

Edward Hart  
Technical Info. Specialist  
STIC/Biotech  
CMI 6B02 Tel: 305-9203

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 9/14/02  
Date Completed: 9/18/02  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_ /  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: XPL  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

GenCore version 4.5  
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## Om nucleic - nucleic search, using sw model

Run on: September 18, 2002, 00:00:48 ; Search time 2325.86 Seconds

US-0-008-789-3

Perfect score: 1755

Sequence: 1 cgcggggcaggccaaaa.....aaaaaaa.....aaaaaaa.....aaaaaaa 1755

Scoring table:

IDENTITY\_NUC Gapop 1.0 , Gapext 1.0

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_bb:\*

2: gb\_hg9:\*

3: gb\_in:\*

4: gb\_on:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_pnt:\*

8: gb\_pnt:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_v1:\*

15: em\_bb:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_cm:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_v1:\*

30: em\_htg\_hum:\*

31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htg\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Match Length	DB ID	Description
------------	-------	--------------	-------	-------------

RESULT 1 AR079463 LOCUS AR079463 DEFINITION Sequence 14 from patent US 5965541. 48 bp DNA ACCESION AR079463 VERSION GI:10006207 KEYWORDS SOURCE ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 48)  
AUTHORS Wickham,T.J., Kovacs,I. and Brough,D.E.  
TITLE Vectors and methods for gene transfer to cells  
PATENT: US 5965541A 14-12-OCR-1999;  
FEATURES source  
source  
Location/Qualifiers 1..48  
KEYWORDS SOURCE ORIGIN /organism="unknown"  
BASE COUNT 30 a 4 c 6 g 8 t  
Query Match Similarity 1.7% Score 30.6; DB 6; Length 48;  
Best Local Similarity 80.0%; Pred. No. 2.2e+04;

GenCore version 4.5  
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## OM nucleic - nucleic search, using sw model

Run on: September 18, 2002, 01:22:31 ; Search time 217.49 Seconds  
(without alignments)  
13854.360 Million cell updates/sec

Title: US-10-008-789-3

Perfect score: 1755

Sequence: cgcggcgaggccaaaa.....aaaaaaaaaaaaaaaaaa 1755

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1905168

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%,

Maximum Match 100%,  
Listing first 45 summaries

Database : N\_Geneseq\_032802.\*

1: /STD51/gcadata/geneseq/geneseq -emb1/NA1980.DAT: \*  
2: /STD51/gcadata/geneseq/geneseq -emb1/NA1981.DAT: \*  
3: /STD51/gcadata/geneseq/geneseq -emb1/NA1982.DAT: \*  
4: /STD51/gcadata/geneseq/geneseq -emb1/NA1983.DAT: \*  
5: /STD51/gcadata/geneseq/geneseq -emb1/NA1984.DAT: \*  
6: /STD51/gcadata/geneseq/geneseq -emb1/NA1985.DAT: \*  
7: /STD51/gcadata/geneseq/geneseq -emb1/NA1986.DAT: \*  
8: /STD51/gcadata/geneseq/geneseq -emb1/NA1987.DAT: \*  
9: /STD51/gcadata/geneseq/geneseq -emb1/NA1988.DAT: \*  
10: /STD51/gcadata/geneseq/geneseq -emb1/NA1989.DAT: \*  
11: /STD51/gcadata/geneseq/geneseq -emb1/NA1990.DAT: \*  
12: /STD51/gcadata/geneseq/geneseq -emb1/NA1991.DAT: \*  
13: /STD51/gcadata/geneseq/geneseq -emb1/NA1992.DAT: \*  
14: /STD51/gcadata/geneseq/geneseq -emb1/NA1993.DAT: \*  
15: /STD51/gcadata/geneseq/geneseq -emb1/NA1994.DAT: \*  
16: /STD51/gcadata/geneseq/geneseq -emb1/NA1995.DAT: \*  
17: /STD51/gcadata/geneseq/geneseq -emb1/NA1996.DAT: \*  
18: /STD51/gcadata/geneseq/geneseq -emb1/NA1997.DAT: \*  
19: /STD51/gcadata/geneseq/geneseq -emb1/NA1998.DAT: \*  
20: /STD51/gcadata/geneseq/geneseq -emb1/NA1999.DAT: \*  
21: /STD51/gcadata/geneseq/geneseq -emb1/NA2000.DAT: \*  
22: /STD51/gcadata/geneseq/geneseq -emb1/NA2001A.DAT: \*  
23: /STD51/gcadata/geneseq/geneseq -emb1/NA2001B.DAT: \*  
24: /STD51/gcadata/geneseq/geneseq -emb1/NA2002.DAT: \*

## ALIGNMENTS

RESULT 1  
ID AAH20344.C  
ID AAH20344 standard: DNA: 40 BP.  
XX  
AC AAH20344:  
XX DT 01-AUG-2001 (first entry)  
XX DE HHV6 virus p41 gene specific primer p41FH373 SEQ ID 25.  
XX PR Primer; solid phase amplification of DNA template; SPRDT; detection; RGP;  
KW genomic scanning; bacterial diagnostic; p41; HHV6; ss.  
XX OS Human herpesvirus 6.  
OS Synthetic.  
PN US6221635-B1.  
XX PD 24-APR-2001.  
XX PF 06-MAY-1999; 99US-0306290.  
PR 06-MAY-1999; 99US-0306290.  
PA (WIST-) WISTAR INST.  
XX Roverta G, Mukhopadhyay S;  
XX DR WPI; 2001-31557/33.  
XX PT Detecting the presence of a specific nucleic acid in a sample containing DNA, useful in scanning large genomic fragments for the  
PT PCR primer, BAR-G

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
C 1	208	1.6	40 22 AAH20344	HHV6 virus p41 gen Human SNP oligonuc
C 2	26.6	1.5	.46 22 AAL28897	Human SNP oligonuc
C 3	26.4	1.5	40 22 AAH20360	HHV6 virus p41 gen
C 4	26.5	1.5	45 22 AAL32265	Human SNP oligonuc
C 5	25.6	1.5	37 19 AAV12343	Ribonucleotide red
C 6	25.6	1.5	44 22 AAL28737	Human SNP oligonuc
C 7	24.8	1.4	47 20 AR20118	Probe for human PG
C 8	24.6	1.4	40 22 AAH20340	HHV6 virus p41 gen
C 9	24.4	1.4	40 24 AAD22099	PCR primer, BAR-G

XX	PT	cancer, autoimmune diseases and infections
PS	PS	Claim 1; Page 1984; 4143pp; English.
CC	CC	The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grove's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms.
CC	CC	XX
CC	CC	SQ Sequence 46 BP; 9 A; 4 C; 3 G; 30 T; 0 other;
XX	XX	Query Match 1.5%; Score 26.6; DB 22; Length 46; Best Local Similarity 78.0%; Pred. NO. 4.4e+03; Matches 32; Conservat. 0; Mismatches 9; Indels 0; Gaps 0;
XX	XX	QY 1714 aataataatccctcgaggtttacaaaaaaaaaaaaaaaaaaaaaa 1754
XX	XX	Db 45 ATTAANAGATTGTTGTCTAACAAKAAAANAAA 5
RESULT 3	AAH20360/C	AAH20360 standard; DNA; 40 BP.
XX	XX	AC AAH20360;
XX	XX	DT 01-AUG-2001 (first entry)
XX	XX	DE HHV6 virus p41 gene specific primer HHV8RP1191 SEQ ID 41.
XX	XX	KW primer; solid phase amplification of DNA template; SPADT; detection; RGP; genomic scanning; bacterial diagnostic; p41; HHV6; ss.
XX	XX	OS Human herpesvirus 6.
OS	Synthetic.	
XX	PN US6221635-B1.	
XX	PD 24-APR-2001.	
XX	PF 06-MAY-1999; 99US-0306290.	
XX	PR 05-MAY-1999; 99US-0306290.	
XX	PA (WIST-) WISTAR INST.	
XX	PI Rovera G, Mukhopadhyay S;	
XX	DR WPI; 2001-315577/33.	
XX	PS Example 2; Column 28; 49pp; English.	Detecting the presence of a specific nucleic acid in a sample containing DNA, useful in scanning large genomic fragments for the presence of genes or gene families, comprises performing solid phase amplification of DNA template -
PS	PS	This invention relates to a method for detecting the presence of a specific nucleic acid in a sample containing DNA. The method comprises performing solid phase amplification of DNA template (SPADT). 5' and 3'

primers are irreversible bound to a solid support, and the DNA from a sample is absorbed and reversibly bound, incubated under amplification reaction conditions and the presence of the specific target DNA is detected. The method is useful for detecting the presence of a specific nucleic acid (e.g. bacterial, viral or parasitic DNA) in a sample or in a cell. SPADT may be used for scanning large genomic fragments for the presence of genes or gene families; or for bacterial diagnostics by examining the ribosomal RNA genes; or for viral diagnostics by scanning for the presence of viral nucleic acid sequences in a sample. SPADT may also be used in forensic medicine by detecting and identifying species specific sequences or for the presence of major histocompatibility complex. The present sequence represents a primer specific for the human herpesvirus 6 (HHV6) p41 gene. The primer is used in an example illustrating the method of the invention.

Sequence 40 BP: 7 A; 2 C; 6 G; 25 T; 0 other;

Query Match 1.5%; Score 26.4; DB 22; Length 40;

Best Local Similarity 83.3%; Pred. No. 4.7e+03; Matches 30; Conservative 0; Mismatches 6; Indels 0; Caps 0;

Oy 1719 taatccctcgagtttacaaaaaaaaaaaaaaaaa 1754  
Db 36 TAACCCCTGATTGAAAAA 1

RESULT 4

ID AAL3265/c  
ID AAL3265 standard; DNA; 45 BP.

AC XX  
AC AAL3265;

XX DT 24-JAN-2002 (first entry)

XX DE Human SNP oligonucleotide #5473.

XX KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinesin; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection; nervous system disease; ss. KW OS Homo sapiens.  
XX KW PN WO200147944-A2.  
XX KW PD 05-JUL-2001.  
XX PF 28-DEC-2000; 2000WO-US35498.

XX PR 28-DEC-1999; 99US-0173419.  
PR 27-DEC-2000; 2000US-0173419.

PA (CURA+) CURAGEN CORP.  
XX PI Shimkets RA, Leach M;  
XX DR WPI: 2001-465210/50.

XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections -  
PT Claim 1: Page 2962: 4143pp; English.  
CC The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amylid proteins, angiopoietin, apopposis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related

proteins, cytochromes, kinesins, cytokines, interleukins, G-protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukemia), diseases of the nervous system and an infection of pathogenic organisms.

Sequence 45 BP: 7 A; 2 C; 5 G; 31 T; 0 other;

Query Match 1.5%; Score 26; DB 22; length 45;

Best Local Similarity 76.2%; Pred. No. 6.1e+03; Matches 32; Conservative 0; Mismatches 10; Indels 0; Caps 0;

Oy 1714 aataataatccctcgagtttacaaaaaaaaaaaaaaaaa 1755  
Db 43 ATAAACACAAACCTAGTTGTGAAAAAA 2

RESULT 5

ID AAV12343  
ID AAV12343 standard; DNA; 37 BP.

AC XX  
AC AAV12343;

XX DT 17-JUN-1998 (first entry)

XX DE Ribonucleotide reductase R2 3' UTR fragment SEQ ID NO:42.

XX KW Ribonucleotide reductase R2; 3'-untranslated region; 3'UTR; tumour; housekeeping gene; identification; modulator; metastasis; neoplastic; papilloma; atherosclerosis; angiogenesis; viral infection; ss. OS Homo sapiens.

XX PN WO980532-A2.

XX PD 08-JAN-1998.

XX PF 30-JUN-1997; 97WO-CA00454.

XX PR 01-JUL-1996; 96US-0021152.

XX PA (WRIG) WRIGHT J A.  
PA (YOUNG) YOUNG A H.

XX PI Wright JA, Young AH;

XX DR WPI: 1998-086958/0B.

XX PT New oligo-nucleotide(s) complementary to untranslated regions of housekeeping genes - are useful in, e.g. identifying modulators of tumour growth/metastasis and inhibiting growth of neoplastic cells

XX PS Claim 7: Page 32; 64pp; English.

CC The present sequence represents a 3'-untranslated region (3'UTR) fragment of ribonucleotide reductase R2. The present invention describes: (1) oligonucleotides (ON) comprising at least 7 consecutive nucleotides (nt) or their analogues of a UTR of a housekeeping gene; (2) antisense ON (AON) complementary to ON; (3) ribozymes (Rb) complementary or homologous to ON, and able to cleave it; (4) DNA sequence encoding ON, OAN and Rb; (5) an antibody (Ab) that binds to ON, OAN and Rb; (6) a nt probe ntp that hybridise to ON, OAN and Rb. ON, OAN, Rb and Ab are used to modulate (especially inhibit) growth of tumour cells (especially neoplastic cells) and to reduce their capacity for metastasis. The above may also be used to treat benign proliferative disorders e.g. papillomas, atherosclerosis,

CC angiogenesis and viral infections, e.g. human immunodeficiency virus, hepatitis or herpes. On may further be used: (i) to identify modulators of tumour growth/metastasis; (ii) to identify compounds (especially potential antitumour agents) that inhibit or enhance interaction between ON and its binding substances; (iii) as probes for detecting related sequences, and (iv) to generate Ab, used for detection and quantification of mAb especially for monitoring progress of cancer therapy. So inhibit tumorigenicity of neoplastic cells, particularly where these are resistant to hydroxyurea.

Sequence 37 BP; 27 A; 3 C; 2 G; 5 T; 0 other:

Query Match 1.5%; Score 25.6; DB 19; Length 37;  
Best Local Similarity 87.5%; Pred. No. 7.1e+03;  
Matches 28; Conservative 0; Mismatches 4;  
Indels 0; Gaps 0;

Oy 1724 cctcgaggttacaaaaaaaaaaaaaaaaa 1755  
2 ccctggatgtccataaaaaaaaaaaaaaaaaa 33

RESULT 6

AAL28737/c  
ID AAL28737 standard; DNA; 44 BP,

XX AC  
XX AAL28737;

DT 24-JAN-2002 (first entry)

XX EIE Human SNP oligonucleotide #1945.

XX KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; KW amyloid protein; angiopoletin; apoptosis related Protein; Cadherin; KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; KW complement related protein; cytochrome; kinase; cytokine; interferon; KW interleukin; G-protein coupled receptor; thioesterase; inflammation; KW multifactorial disease; autoimmune disease; infection; KW nervous system disease; ss.

XX US Homo sapiens.

XX PN WO200147944-A2.

XX PD 05-JUL-2001.

XX PF 28-DEC-2000; 2000WO-US35498.

XX PR 28-DEC-1999; 99US0173419.

XX PR 27-DEC-2000; 2000US0173419.

XX PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Leach M;

XX DR WPI; 2001-465210/50.

XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.

XX PS Claim 1; Page 1937; 4143pp; English.

The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoletin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinases, cytokines, interferons, interleukins and G-protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed

CC above, disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, cancer systemic lupus erythematosus and Grave's disease); inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms.

XX Sequence 44 BP; 11 A; 1 C; 4 G; 28 T; 0 other;

Query Match 1.5%; Score 25.6; DB 22; Length 44;  
Best Local Similarity 77.5%; Pred. No. 7.6e+03;  
Matches 31; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 1716 tataatccctcggttacaaaaaaaaaaaaaaaaa 1755  
41 TATTAAATCCAGTATTCAAAAAAAA 2

RESULT 7

AAZ011B  
ID AAZ011B Standard; DNA; 47 BP,

XX AC  
XX AAZ011B;

XX DT 27-SEP-1999 (first entry)

XX DE Probe for human PG1 biallelic marker 4-4-187.

XX PG1 gene; biallelic marker; PCR Primer; PG1-related biallelic marker; KW cancer; prostate cancer; diagnosis; therapy; prostate specific antigen; KW PSA; human; ss.

XX OS Synthetic.

OS Homo sapiens.

XX PN WO9326644-A2.

XX PR 09-SEP-1998; 98US049658.

XX PR 22-DEC-1997; 97US-0996316.

XX PA (GEST ) GENSET.

XX PI Blumenthal M, Bouquerel L, Chumakov I, Cohen D;

XX DR WPI; 1999-405178/34.

XX PT Use of a prostate cancer associated gene and biallelic markers

PT derived from it

XX PS Claim 4; Page 325; 385pp; English.

XX The invention relates to a mammalian PG1 gene and protein, and a set of CC PGL biallelic markers. The PGL polynucleotide and biallelic markers are CC used in a hybridisation assay, a sequencing assay, or in an CC allele-specific amplification assay for determining the identity of a CC nucleotide at a PGL-related biallelic marker. The methods can be used to CC detect and to assess the risk of developing cancer or prostate cancer. CC Early-stage diagnosis of prostate cancer relies on prostate specific CC antigen (PSA) dosage. However, the effectiveness of this is limited due CC to its inability to discriminate between malignant and non-malignant CC afflictions of the organ. A need exists for both a reliable diagnostic CC procedure which would enable early-stage diagnosis, and for preventative CC and curative treatments of the disease. The PGL gene can be used for CC detection of prostate cancer, and the risk of developing it in the future, and can also be used to determine therapies for the disease.

XX Sequence 47 BP; 34 A; 2 C; 5 G; 6 T; 0 other;



CC determine presence or absence of predisposing disease haplotypes such as colon cancer, breast cancer, neurofibromatosis type 2, cystic fibrosis, thalassaemia and phenylketonuria. Identification of haplotypes associated with phenotypic traits is useful for identifying predisposition to disease. The methods are also useful in prenatal screening to identify whether a foetus is afflicted with or is predisposed to develop a serious disease. The present DNA sequence is PCR primer, BAR-G used for haplotyping hybridisation in the exemplification of the invention.

Sequence 40 BP; 6 A; 6 C; 3 G; 25 T; 0 other;

Query Match 1.4%; Score 24.4; DB 24;  
Best Local Similarity 82.4%; Pred. No. 1.4e+04;  
Matches 28; Conservative 0; Mismatches 6;  
Indels 0; Gaps 0;

Oy 1722 tccttcgatttcaaaaaaaaaaaaaaaa 1755  
Db 34 TCCATGGGTGAAAAAAAAA 1

RESULT 10

AAD1285  
ID AAD1285 standard; DNA; 40 BP.

XX  
AC AAD1285:  
XX  
DT 24-SEP-2001 (first entry)

RE Mycobacterium 16S rRNA capture oligomer.  
XX  
KW Mycobacterium; 16S ribosomal RNA; amplification;  
OS Mycobacterium sp.

XX  
FH Key modified\_base  
FT 1 /\*tag= a  
FT /mod\_base= gm  
FT modified\_base  
FT 2 /\*tag= b  
FT /mod\_base= cm  
FT modified\_base  
FT 3 /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxy-thymidine"  
FT modified\_base  
FT 4 /\*tag= d  
FT /mod\_base= gm  
FT modified\_base  
FT 5 /\*tag= e  
FT /mod\_base= OTHER  
FT modified\_base  
FT 6 /\*tag= f  
FT /mod\_base= gm  
FT modified\_base  
FT 7 /\*tag= g  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxy-thymidine"  
FT 8 /\*tag= h  
FT /mod\_base= gm  
FT modified\_base  
FT 9..11 /\*tag= i  
FT /mod\_base= gm  
FT modified\_base  
FT 12 /\*tag= j  
FT /mod\_base= gm  
FT modified\_base  
FT 13 /\*tag= k  
FT /mod\_base= gm

Length 40;  
XX  
PR 17-DEC-1999; 99WO-US30346.  
XX  
PR 17-DEC-1999; 99WO-US30346.

PA (GENP) GEN-PROBE INC.  
PA (INMR) BIOMERIEUX SA.  
XX  
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;  
XX  
WPI: 2001-398170/42.

XX  
PT Detecting Mycobacterium species, involves in vitro amplification of 16S rRNA or DNA encoding RNA in nucleic acid amplification mixture using PT specific primers, and detecting the amplified nucleic acid

XX  
PS Example 6: Page 39; 44PP: English.

CC The invention relates to a method of detecting Mycobacterium species, CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA encoding 16S rRNA in an in vitro nucleic acid amplification mixture comprising two primers, and then detecting the amplified nucleic acid. The method is relatively simple and useful for detecting the presence of various Mycobacterium species in a biological sample, and thus important for diagnosis of infections resulting from them. The method is especially important for screening opportunistic infections caused by M. tuberculosis or a Mycobacterium other than tuberculosis (MOTT). The present sequence is a capture CC oligomer that includes a sequence that specifically binds to the CC Mycobacterium rRNA target sequence and a 3' poly-A tail sequence CC complementary to an immobilised sequence for capturing the target rRNA on a solid support.

XX  
Sequence 48 BP; 32 A; 5 C; 3 G; 8 T; 0 other;  
Query Match 1.4%; Score 24.4; DB 22;  
Best Local Similarity 82.4%; Pred. No. 1.5e+04;  
Matches 28; Conservative 0; Mismatches 6;  
Indels 0; Gaps 0;

Oy 1722 tccttcgatttcaaaaaaaaaaaaaaaa 1755  
Db 7 tgccgtatttaaaaaaa 40

RESULT 11

AZ223473  
ID AZ23473 standard; DNA; 42 BP.

XX  
AC AZ23473:  
XX  
DT 20-JAN-2000 (first entry)

XX  
DE A. thaliana at-cbfl gene PCR primer cbfl-forward 1.  
XX  
KW Environmental stress tolerance; Plant; binding protein; DNA regulation;  
KW CBF1; C-repeat/DRE binding factor; CGG regulatory sequence; COR; cold;  
KW cold-related gene; drought; high salinity; tissue-specific promoter;

FT /\*tag= k  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxy-thymidine"  
FT 14  
FT /\*tag= l  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxy-adenosine"  
FT 15  
FT /\*tag= m  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxy-thymidine"  
FT XX  
PR WO20014510-A2.  
XX  
PD 21-JUN-2001.  
XX  
PR 17-DEC-1999; 99WO-US30346.  
XX  
PR 17-DEC-1999; 99WO-US30346.  
XX  
PA (GENP) GEN-PROBE INC.  
PA (INMR) BIOMERIEUX SA.  
XX  
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;  
XX  
WPI: 2001-398170/42.

XX  
PT Detecting Mycobacterium species, involves in vitro amplification of 16S rRNA or DNA encoding RNA in nucleic acid amplification mixture using PT specific primers, and detecting the amplified nucleic acid

XX  
PS Example 6: Page 39; 44PP: English.

CC The invention relates to a method of detecting Mycobacterium species, CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA encoding 16S rRNA in an in vitro nucleic acid amplification mixture comprising two primers, and then detecting the amplified nucleic acid. The method is relatively simple and useful for detecting the presence of various Mycobacterium species in a biological sample, and thus important for diagnosis of infections resulting from them. The method is especially important for screening opportunistic infections caused by M. tuberculosis or a Mycobacterium other than tuberculosis (MOTT). The present sequence is a capture CC oligomer that includes a sequence that specifically binds to the CC Mycobacterium rRNA target sequence and a 3' poly-A tail sequence CC complementary to an immobilised sequence for capturing the target rRNA on a solid support.

KW	PCR primer; at-cbfl; ss.
OS	Synthetic.
OS	Arabidopsis thaliana.
XX	W0998977-R2.
PN	
XX	PD 05-AUG-1999.
XX	XX PF 28-JAN-1999; 99WO-US01895.
XX	XX PR 03-FEB-1998; 98US-001755.
PR	03-FEB-1998; 98US-001781.
PR	03-FEB-1998; 98US-0018237.
PR	03-FEB-1998; 98US-001833.
PR	03-FEB-1998; 98US-0018334.
PR	03-FEB-1998; 98US-0018235.
PR	23-NOV-1998; 98US-0198119.
PA	(MENDL-) MENDEL BIOTECHNOLOGY INC.
PA	(UNMS ) UNIV MICHIGAN STATE.
XX	PT Environmental stress tolerance gene binding proteins useful for altering plant stress tolerance -
XX	PI Stockinger EJ, Jaglo-Ottosen K, Zarka D, Gilmour SJ, Jiang C;
XX	PT Fromm M, Thomashow MF;
XX	DR WPI: 1999-561312/47.
XX	PS Example 4c: Page 181, 252pp; English.
XX	This invention describes novel binding proteins other than CBF-1 (C-repeat/DRE binding factor) in isolated form which comprise a consensus sequence capable of binding to a CG regulatory sequence. The binding proteins are capable of binding to a DNA regulatory sequence, which regulates expression of one or more environmental stress tolerance genes, especially COR (cold-related) genes. Environmental stress may be, e.g. cold temperatures, drought and high salinity. Plants transformed with the binding protein (or sequences encoding it) can have altered environmental stress tolerance. The binding protein coding sequences can be under the control of tissue-specific promoters. AAZ23472-223475 represent PCR primers used in the amplification of the Arabidopsis thaliana at-cbfl gene described in the method of the invention.
SO	Sequence 42 BP: 18 A; 9 C; 5 G; 10 T; 0 other;
SO	Query Match 1.4%; Score 23.8; DB 20; Length 42; Best Local Similarity 80.0%; Pred. No. 2e-04; Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY	1721 atccctcgatgttacaaaaaaa 1755
Db	6 atccctcgatgttacaaaaaaaataaaa 40
RESULT 12	Query Match 1.4%; Score 23.8; DB 22; Length 45; Best Local Similarity 92.6%; Pred. No. 2.1e-04; Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
AAL28218/C	OY 1729 agtttacaaaaaaa 1755
ID AAL28218 standard; DNA; 45 BP.	Db 30 AATTACAAATTAANAAA 4
AC AAL28218;	RESULT 13
XX	AAL28459/C
DT 24-JAN-2002 (first entry)	TD AAT28459 standard; DNA; 46 BP.
DE Human SNP oligonucleotide #1426.	XX AC AAL28459;
XX	XX DT 24-JAN-2002 (first entry)
DE Human SNP oligonucleotide #1667.	XX DE Human SNP oligonucleotide #1667.
XX	KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinesin; cytokine; interferon; complement related protein; cytochrome; kinesin; cytokine; interferon; multifactorial disease; autoimmune disease; infection;

XX	narvous system disease;	ss.
OS	Homo sapiens.	
XX		
PN	WO200147944-A2.	
XX		
PD	05-JUL-2001.	
XX		
PR	28-DEC-2000: 2000WO-US35498.	
XX		
PR	28-DEC-1999; 99US-0173419.	
XX		
PR	27-DEC-2000: 2000US-0173419.	
XX		
PA	(CURA-) CURAGEN CORP.	
XX		
PI	Shimkets RA, Leach M;	
XX		
DR	WPI: 2001-465210/50.	
XX		
PR	Polymerropic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections -	
XX		
PS	Claim 1; Page 1857; 4143pp; English.	
XX		
CC	The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, cancer leukaemia), diseases of the nervous system and an infection of pathogenic organisms.	
XX		
SQ	Sequence 46 BP; 4 A; 3 C; 3 G; 36 T; 0 other;	
XX		
Query Match	1.4%; Score 23.8; DB 22; Length 46;	
' Best Local Similarity	92.6%; Pred. No. 2.1e+04;	
Matches 25; Conservative	0; Mismatches 2;	
Indels 0; Gaps 0;		
Oy	1729 agttttcaaaaaaaaaaaaaaaa 1755	
Db	27 ATTAACAAAAA 1	
XX		
RESULT 14		
AAL29941/C		
ID AAL29941 standard; DNA; 47 BP.		
XX		
AC	AAL29941;	
XX		
DT	24-JAN-2002 (first entry)	
XX		
DE	Human SNP oligonucleotide #3149.	
XX		
KW	Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopeptin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinesin; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection; nervous system disease; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200147944-A2.	
XX		
PD	05-JUL-2001.	
XX		
PR	28-DEC-2000: 2000WO-US35498.	
XX		
PR	28-DEC-1999; 99US-0173419.	
XX		
PR	27-DEC-2000; 2000US-0173419.	
XX		
PA	(CURA-) CURAGEN CORP.	
XX		
PI	Shimkets RA, Leach M;	
XX		
DR	WPI: 2001-465210/50.	
XX		
PT	Polymerropic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections -	
XX		
PS	Claim 1; Page 2289; 4143pp; English.	
XX		
CC	The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, cancer leukaemia), diseases of the nervous system and an infection of pathogenic organisms.	
CC		
CC	Sequence 47 BP; 10 A; 4 C; 2 G; 31 T; 0 other;	
XX		
Query Match	1.4%; Score 23.8; DB 22; Length 47;	
' Best Local Similarity	92.6%; Pred. No. 2.1e+04;	
Matches 25; Conservative	0; Mismatches 2;	
Indels 0; Gaps 0;		
Oy	1729 agttttcaaaaaaaaaaaaaaaa 1755	
Db	28 AGCTAACAAAAAA 2	
XX		
RESULT 15		
AAT43897/C		
ID AAT43897 standard; DNA; 38 BP.		
XX		
AC	AAT43897;	
XX		
DT	10-MAR-2000 (first entry)	
XX		
DE	M. tuberculosis rpo-beta primer 10.	
XX		
KW	RNA polymerase; rpo-beta; detection; diagnostic; trap probe; primer; ss.	
XX		
OS	Mycobacterium tuberculosis.	
XX		
PN	EP62536-A1.	
XX		
PD	08-DEC-1999.	
XX		
PF	29-MAY-1999; 99EP-0110458.	
XX		
PR	04-JUN-1998; 98DE-1024900.	

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PA  
XX  
(HOFF ) ROCHE DIAGNOSTICS GMBH.

PT  
XX  
Weindel K., Brand J;

DR  
XX  
PT  
XX  
Selective detection of nucleic acids by amplification with labeled

primers and detection with a trap probe

PS  
XX  
Example 1c: Page 18; 27pp; German.

This invention describes a novel method for the selective detection of nucleic acids which comprises amplification of the nucleic acid with the help of labeled primers and detection with a trap probe. The methods and reagents are used for the detection of a marker primer and at least 2 immobilized (or immobilizable) trap probes with the corresponding nucleic acid sequence of interest for mutation analysis. The method can be used to detect a specific sequence in a sample of one or more nucleic acids by using several sets of primers and trap probes (i.e. in an array). The methods are useful in molecular biology and diagnostic applications, especially for simultaneous detection of multi-pathogens, typing of organisms, analyzing genetic diversity and sequencing of genes or genomes. This sequence represents a primer used in the method of the invention.

CC  
XX  
SQ

Sequence 38 BP; 4 A; 7 C; 5 G; 22 T; 0 other;

Query Match 1.3%; Score 23 6; DB 21; Length 38:

Best Local Similarity 86.7%; Score 23 6; DB 21; Length 38:  
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1726 tcgggtttccaaaaaaaabaaaaaa 1755  
||| ||| ||| ||| ||| ||| ||| |||  
Db 30 TCGGGTTGAAAAAAAGAAAAA 1

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Job time: 783 sec